

PATENT  
GENENT.2827A2  
Date: January 11, 2001

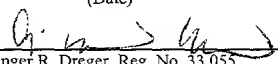
**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Applicant(s) : Pennica et al.  
Appl. No. : Unknown  
Filed : Filed Herewith  
For : NOVEL STRA6  
POLYPEPTIDES  
Examiner : Unknown  
Group Art Unit : Unknown

I hereby certify that this correspondence and all  
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an envelope addressed to: Assistant Commissioner  
for Patents, Washington, D.C. 20231, on

January 11, 2001

(Date)

  
Ginger R. Dreger, Reg No 33,055

SEQUENCE SUBMISSION STATEMENT

Assistant Commissioner for Patents  
Washington, D.C. 20231

Dear Sir:

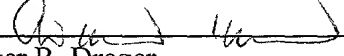
I hereby state that the information recorded in computer readable form is identical to the  
written sequence listing submitted herewith as required in 37 CFR § 1.821(f) and (g).

I further state that this submission includes no new matter.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: January 11, 2001

By:   
Ginger R. Dreger  
Registration No. 33,055  
Attorney of Record

# SEQUENCE LISTING

<110> Pennica, Diane  
Smith, Victoria  
Wood, William I.

<120> Novel STRA6 Polypeptides

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Phe Gly Ile Val Leu Ser Glu Asp Lys Gln Glu Val Val Glu Leu Val			
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Glu Tyr Leu Arg Asn Leu Leu Cys Arg Lys Lys Leu Gly Ser Ser Tyr	
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Val Leu Ser Ala Thr Leu Thr Gly Thr Ala Ile Tyr Gln Val Ala Leu	
290	295 300
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Leu Leu Leu Val Gly Val Val Pro Thr Ile Gln Lys Val Arg Ala Gly	
305	310 315
gtc acc acg gat gtc tcc tac ctg ctg gcc ggc ttt gga atc gtg ctc	1190
Val Thr Thr Asp Val Ser Tyr Leu Leu Ala Gly Phe Gly Ile Val Leu	
320	325 330 335
tcc gag gac aag cag gag gtg gtg gag ctg gtg aag cac cat ctg tgg	1238
Ser Glu Asp Lys Gln Glu Val Val Glu Leu Val Lys His His Leu Trp	
340	345 350
gct ctg gaa gtg tgc tac atc tca gcc ttg gtc ttg tcc tgc tta ctc	1286
Ala Leu Glu Val Cys Tyr Ile Ser Ala Leu Val Leu Ser Cys Leu Leu	
355	360 365
acc ttc ctg gtc ctg atg cgc tca ctg gtg aca cac agg acc aac ctt	1334
Thr Phe Leu Val Leu Met Arg Ser Leu Val Thr His Arg Thr Asn Leu	
370	375 380
cga gct ctg cac cga gga gct gcc ctg gac ttg agt ccc ttg cat cgg	1382
Arg Ala Leu His Arg Gly Ala Ala Leu Asp Leu Ser Pro Leu His Arg	
385	390 395
agt ccc cat ccc tcc cgc caa gcc ata ttc tgt tgg atg agc ttc agt	1430
Ser Pro His Pro Ser Arg Gln Ala Ile Phe Cys Trp Met Ser Phe Ser	
400	405 410 415
gcc tac cag aca gcc ttt atc tgc ctt ggg ctc ctg gtg cag cag atc	1478
Ala Tyr Gln Thr Ala Phe Ile Cys Leu Gly Leu Leu Val Gln Gln Ile	

420	425	430	
atc ttc ttc ctg gga acc acg gcc ctg gcc ttc ctg gtg ctc atg cct Ile Phe Phe Leu Gly Thr Thr Ala Leu Ala Phe Leu Val Leu Met Pro 435 440 445			1526
gtg ctc cat ggc agg aac ctc ctg ctc ttc cgt tcc ctg gag tcc tcg Val Leu His Gly Arg Asn Leu Leu Leu Phe Arg Ser Leu Glu Ser Ser 450 455 460			1574
tgg ccc ttc tgg ctg act ttg gcc ctg gct gtg atc ctg cag aac atg Trp Pro Phe Trp Leu Thr Leu Ala Leu Ala Val Ile Leu Gln Asn Met 465 470 475			1622
gca gcc cat tgg gtc ttc ctg gag act cat gat gga cac cca cag ctg Ala Ala His Trp Val Phe Leu Glu Thr His Asp Gly His Pro Gln Leu 480 485 490 495			1670
acc aac cgg cga gtg ctc tat gca gcc acc ttt ctt ctc ttc ccc ctc Thr Asn Arg Arg Val Leu Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu 500 505 510			1718
aat gtg ctg gtg ggt gcc ata gtg gcc acc tgg cga gtg ctc ctc tct Asn Val Leu Val Gly Ala Ile Val Ala Thr Trp Arg Val Leu Leu Ser 515 520 525			1766
gcc ctc tac aac gcc atc cac ctt ggc cag atg gac ctc agc ctg ctg Ala Leu Tyr Asn Ala Ile His Leu Gly Gln Met Asp Leu Ser Leu Leu 530 535 540			1814
cca ccg aga gcc gcc act ctc gac ccc ggc tac tac acg tac cga aac Pro Pro Arg Ala Ala Thr Leu Asp Pro Gly Tyr Thr Tyr Arg Asn 545 550 555			1862
ttc ttg aag att gaa gtc agc cag tcg cat cca gcc atg aca gcc ttc Phe Leu Lys Ile Glu Val Ser Gln Ser His Pro Ala Met Thr Ala Phe 560 565 570 575			1910
tgc tcc ctg ctc ctg caa gcg cag agc ctc cta ccc agg acc atg gca Cys Ser Leu Leu Leu Gln Ala Gln Ser Leu Leu Pro Arg Thr Met Ala 580 585 590			1958
gcc ccc cag gac agc ctc aga cca ggg gag gaa gac gaa ggg atg cag Ala Pro Gln Asp Ser Leu Arg Pro Gly Glu Glu Asp Glu Gly Met Gln 595 600 605			2006
ctg cta cag aca aag gac tcc atg gcc aag gga gct agg ccc ggg gcc Leu Leu Gln Thr Lys Asp Ser Met Ala Lys Gly Ala Arg Pro Gly Ala 610 615 620			2054
agc cgc ggc agg gct cgc tgg ggt ctg gcc tac acg ctg ctg cac aac Ser Arg Gly Arg Ala Arg Trp Gly Leu Ala Tyr Thr Leu Leu His Asn 625 630 635			2102
cca acc ctg cag gtc ttc cgc aag acg gcc ctg ttg ggt gcc aat ggt Pro Thr Leu Gln Val Phe Arg Lys Thr Ala Leu Leu Gly Ala Asn Gly 640 645 650 655			2150

gcc cag ccc t gagggcaggg aagggtcaacc cacctgccca tctgtgctga 2200  
Ala Gln Pro

ggcatgttcc tgccataccac ctctccctc cccggctctc ctcccagcat cacaccagcc 2260  
atgcagccag caggctctcc ggatcaactgt ggttgggtgg aggtctgtct gcactgggag 2320  
cctcaggagg gctctgtctc acccaacttg ctatgggaga gccagcaggg gttctggaga 2380  
aagaaactgg tgggttaggg ccttgggtcca ggagccagtt gagccagggc agccacatcc 2440  
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<210> 5

<211> 658

<212> PRT

<213> Homo sapiens

<400> 5

Met	Ser	Ser	Gln	Pro	Ala	Gly	Asn	Gln	Thr	Ser	Pro	Gly	Ala	Thr	Glu
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Asp	Tyr	Ser	Tyr	Gly	Ser	Trp	Tyr	Ile	Asp	Glu	Pro	Gln	Gly	Gly	Glu
			20					25					30		
Glu	Leu	Gln	Pro	Glu	Gly	Glu	Val	Pro	Ser	Cys	His	Thr	Ser	Ile	Pro
			35				40					45			
Pro	Gly	Leu	Tyr	His	Ala	Cys	Leu	Ala	Ser	Leu	Ser	Ile	Leu	Val	Leu
			50			55					60				
Leu	Leu	Leu	Ala	Met	Leu	Val	Arg	Arg	Arg	Gln	Leu	Trp	Pro	Asp	Cys
65					70					75					80
Val	Arg	Gly	Arg	Pro	Gly	Leu	Pro	Arg	Pro	Arg	Ala	Val	Pro	Ala	Ala
				85					90					95	
Val	Phe	Met	Val	Leu	Leu	Ser	Ser	Leu	Cys	Leu	Leu	Leu	Pro	Asp	Glu
			100					105					110		
Asp	Ala	Leu	Pro	Phe	Leu	Thr	Leu	Ala	Ser	Ala	Pro	Ser	Gln	Asp	Gly
			115				120					125			
Lys	Thr	Glu	Ala	Pro	Arg	Gly	Ala	Trp	Lys	Ile	Leu	Gly	Leu	Phe	Tyr
			130			135					140				
Tyr	Ala	Ala	Leu	Tyr	Tyr	Pro	Leu	Ala	Ala	Cys	Ala	Thr	Ala	Gly	His
145					150					155					160
Thr	Ala	Ala	His	Leu	Leu	Gly	Ser	Thr	Leu	Ser	Trp	Ala	His	Leu	Gly
				165					170					175	
Val	Gln	Val	Trp	Gln	Arg	Ala	Glu	Cys	Pro	Gln	Val	Pro	Lys	Ile	Tyr
			180					185					190		
Lys	Tyr	Tyr	Ser	Leu	Leu	Ala	Ser	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Gly
			195			200						205			
Phe	Leu	Ser	Leu	Trp	Tyr	Pro	Val	Gln	Leu	Val	Arg	Ser	Phe	Ser	Arg
			210			215					220				
Arg	Thr	Gly	Ala	Gly	Ser	Lys	Gly	Leu	Gln	Ser	Ser	Tyr	Ser	Glu	Glu
225					230					235					240
Tyr	Leu	Arg	Asn	Leu	Cys	Arg	Lys	Lys	Leu	Gly	Ser	Ser	Tyr	His	
			245					250						255	
Thr	Ser	Lys	His	Gly	Phe	Leu	Ser	Trp	Ala	Arg	Val	Cys	Leu	Arg	His
			260					265					270		
Cys	Ile	Tyr	Thr	Pro	Gln	Pro	Gly	Phe	His	Leu	Pro	Leu	Lys	Leu	Val

275	280	285
Leu Ser Ala Thr Leu Thr Gly Thr Ala Ile Tyr Gln Val Ala Leu Leu		
290	295	300
Leu Leu Val Gly Val Val Pro Thr Ile Gln Lys Val Arg Ala Gly Val		
305	310	315
Thr Thr Asp Val Ser Tyr Leu Leu Ala Gly Phe Gly Ile Val Leu Ser		
	325	330
		335
Glu Asp Lys Gln Glu Val Val Glu Leu Val Lys His His Leu Trp Ala		
	340	345
		350
Leu Glu Val Cys Tyr Ile Ser Ala Leu Val Leu Ser Cys Leu Leu Thr		
	355	360
		365
Phe Leu Val Leu Met Arg Ser Leu Val Thr His Arg Thr Asn Leu Arg		
	370	375
		380
Ala Leu His Arg Gly Ala Ala Leu Asp Leu Ser Pro Leu His Arg Ser		
385	390	395
Pro His Pro Ser Arg Gln Ala Ile Phe Cys Trp Met Ser Phe Ser Ala		
	405	410
		415
Tyr Gln Thr Ala Phe Ile Cys Leu Gly Leu Leu Val Gln Gln Ile Ile		
	420	425
		430
Phe Phe Leu Gly Thr Thr Ala Leu Ala Phe Leu Val Leu Met Pro Val		
	435	440
		445
Leu His Gly Arg Asn Leu Leu Leu Phe Arg Ser Leu Glu Ser Ser Trp		
	450	455
		460
Pro Phe Trp Leu Thr Leu Ala Leu Ala Val Ile Leu Gln Asn Met Ala		
465	470	475
		480
Ala His Trp Val Phe Leu Glu Thr His Asp Gly His Pro Gln Leu Thr		
	485	490
		495
Asn Arg Arg Val Leu Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu Asn		
	500	505
		510
Val Leu Val Gly Ala Ile Val Ala Thr Trp Arg Val Leu Leu Ser Ala		
	515	520
		525
Leu Tyr Asn Ala Ile His Leu Gly Gln Met Asp Leu Ser Leu Leu Pro		
	530	535
		540
Pro Arg Ala Ala Thr Leu Asp Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe		
545	550	555
		560
Leu Lys Ile Glu Val Ser Gln Ser His Pro Ala Met Thr Ala Phe Cys		
	565	570
		575
Ser Leu Leu Leu Gln Ala Gln Ser Leu Leu Pro Arg Thr Met Ala Ala		
	580	585
		590
Pro Gln Asp Ser Leu Arg Pro Gly Glu Glu Asp Glu Gly Met Gln Leu		
	595	600
		605
Leu Gln Thr Lys Asp Ser Met Ala Lys Gly Ala Arg Pro Gly Ala Ser		
	610	615
		620
Arg Gly Arg Ala Arg Trp Gly Leu Ala Tyr Thr Leu Leu His Asn Pro		
625	630	635
		640
Thr Leu Gln Val Phe Arg Lys Thr Ala Leu Leu Gly Ala Asn Gly Ala		
	645	650
		655
Gln Pro		

1000  
 900  
 800  
 700  
 600  
 500  
 400  
 300  
 200  
 100  
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